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Genome Sequence of an *Enterobacter helveticus* Strain, 1159/04 (LMG 23733), Isolated from Fruit Powder

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We report the draft genome sequence of *Enterobacter helveticus* strain LMG 23733, isolated from fruit powder. The draft genome assembly for *E. helveticus* strain LMG 23733 has a size of 4,635,476 bp and a G+C content of 55.9%.

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Stephan et al. (1) reported the isolation of 12 strains from fruit powder, which were presumptively identified as *Enterobacter sakazakii*, now *Cronobacter*, through the use of differential media. Biochemical characterization revealed that these isolates did not belong to the genus *Cronobacter*. Sequence analysis of the 16S rRNA and *rpoB* genes and DNA-DNA hybridization confirmed this finding, and Stephan et al. (1) classified two of these 12 strains as belonging to the novel species *Enterobacter helveticus*.

Recently, Brady et al. (2) proposed that *E. helveticus* be recognized as a new *Cronobacter* species. Because the taxonomic position of this species has been questioned, we sequenced *E. helveticus* strain 1159/04 (LMG 23733) to address this question. A library was constructed using the Nextera XT DNA sample preparation kit (Illumina, San Diego, CA), and whole-genome sequencing was performed on a MiSeq sequencer (Illumina, San Diego, CA), utilizing 500-cycle paired-end version 2 chemistry. Paired-end FASTQ datasets were trimmed and assembled using CLC Genomics Workbench, version 6.0.5 (CLC bio, Aarhus, Denmark). A draft genome sequence of strain 1159/04 was 4,635,476 bp, on 161 contigs (>500 bp in size). Genomic contigs were annotated using the RAST annotation server (3) to identify RNAs and protein-encoding genes. The draft genome sequence of strain 1159/04 is predicted to contain 4,454 coding sequences (CDS).

This strain of *E. helveticus* is closely related, as revealed by comparative genomics, to the type strain LMG23732 (513/05) as sequenced by Massod et al. (4). Indeed, the average nucleotide identity (ANI) between the two genomes is 99.95%. Both genomes contained a number of noteworthy features, namely, operons for the catabolism of protocatechuate, xylose, xyloside, L-rhamnose, D-galactarate, D-galactonate, malonate, galactitol, putrescine, fructoselysine, and L-idonic acid, as well as the presence of six type I fimbria clusters and one sigma fimbria cluster, genes for curli fimbriae, a transposon harboring copper resistance, redundant zinc transporter operons, a *pga* biofilm operon, and the *lsr* autoinducer-2 operon. Strain 513/05^T harbors a phosphonate degradation operon. Additionally, there are a number of ATP-

binding cassette (ABC)-type transporters of unidentified sugar substrates. The main differences between the two strains were due to the presence of a number of mobile elements. These included a Tn7-like transposon commonly found on plasmids of other *Enterobacteriaceae*, a transposon-like element harboring mercury resistance, an inovirus bacteriophage, and a large (>190-kbp) IncH1 conjugative plasmid, homologous (97 to 99% identity) to the R478 family of group H conjugative plasmids, in the genome of strain 513/05^T (5). Strain 1159/04 harbored a smaller plasmid homologous to IncN2 plasmids shown to carry the New Delhi metallo- β -lactamase gene (6, 7).

Nucleotide sequence accession number. The whole-genome shotgun project for *E. helveticus* strain 1159/04 is available in GenBank under accession number [AXDL00000000](#).

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REFERENCES

- Stephan R, Van Trappen S, Cleenwerck I, Vancanneyt M, De Vos P, Lehner A. 2007. *Enterobacter turicensis*, sp. nov. and *Enterobacter helveticus*, sp. nov., isolated from fruit powder. *Int. J. Syst. Evol. Microbiol.* 57: 820–826.
- Brady C, Cleenwerck I, Venter S, Coutinho T, De Vos P. 2013. Taxonomic evaluation of the genus *Enterobacter* based on multilocus sequence analysis (MLSA): proposal to reclassify *E. nimipressuralis* and *E. amnigenus* into *Lelliottia* gen. nov. as *Lelliottia nimipressuralis* comb. nov. and *Lelliottia amnigena* comb. nov., respectively, *E. gergoviae* and *E. pyrinus* into *Pluralibacter* gen. nov. as *Pluralibacter gergoviae* comb. nov. and *Pluralibacter pyrinus* comb. nov., respectively, *E. cowanii*, *E. radincincitans*, *E. oryzae* and *E. arachidis* into *Kosakonia* gen. nov. as *Kosakonia cowanii* comb. nov., *Kosakonia radincincitans* comb. nov., *Kosakonia oryzae* comb. nov. and *Kosakonia arachidis* comb. nov., respectively, and *E. turicensis*, *E. helveticus* and *E. pulveris* into *Cronobacter* as *Cronobacter zurichensis* nom. nov., *Cronobacter helveticus* comb. nov. and *Cronobacter pulveris* comb. nov., respectively, and emended description of the genera *Enterobacter* and *Cronobacter*. *Syst. Appl. Microbiol.* 36:309–319.

3. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75.
4. Masood N, Moore K, Farbos A, Hariri S, Paszkiewicz K, Dickins B, McNally A, Forsythe S. 2013. Draft genome sequences of three newly identified species in the genus *Cronobacter*, *C. helveticus* LMG23732^T, *C. pulveris* LMG24059, and *C. zurichensis* LMG23730^T. *Genome Announc.* 1(5):e00783-13. doi:[10.1128/genomeA.00783-13](https://doi.org/10.1128/genomeA.00783-13).
5. Gilmour MW, Thomson NR, Sanders M, Parkhill J, Taylor DE. 2004. The complete nucleotide sequence of the resistance plasmid R478: defining the backbone components of incompatibility group H conjugative plasmids through comparative genomics. *Plasmid* 52:182–202.
6. Poirel L, Dortet L, Bernabeu S, Nordmann P. 2011. Genetic features of *bla*NDM-1-positive *Enterobacteriaceae*. *Antimicrob. Agents Chemother.* 55:5403–5407.
7. Chen YT, Lin AC, Siu LK, Koh TH. 2012. Sequence of closely related plasmids encoding *bla*(NDM-1) in two unrelated *Klebsiella pneumoniae* isolates in Singapore. *PLoS One* 7:e48737. doi:[10.1371/journal.pone.0048737](https://doi.org/10.1371/journal.pone.0048737).